This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. – 11. (canceled)

12. (previously presented) A method for screening a candidate compound for the ability to reduce cellular proliferation comprising the steps of:

(a) providing a sublethal level of an antisense nucleic acid complementary to at least a portion of a nucleic acid encoding a gene product in a cell to reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell, wherein said gene product is a gene product whose activity or amount is reduced by an antisense nucleic acid comprising a nucleotide sequence of SEQ ID NO: 1463, provided that cell is a prokaryotic organism;

(b) contacting said sensitized cell with a compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a nonsensitized cell.

13. – 30. (canceled)

31. (currently amended) A method for screening a candidate compound for the ability to reduce cellular proliferation comprising:

(a) providing a sublethal level of an antisense nucleic acid complementary to at least a portion of a nucleic acid encoding a gene product in a cell to reduce the activity or amount of

said gene product in said cell, thereby producing a sensitized cell, provided that said cell is a prokaryotic organism and wherein said gene product is either:

i) encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a polypeptide whose expression is inhibited by an antisense nucleic acid of SEQ ID NO: 1463;

ii) has at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a polypeptide whose expression is inhibited by an antisense nucleic acid of SEQ ID NO: 1463;

iii) encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid of SEQ ID NO: 1463 under stringent conditions, wherein the stringent conditions are hybridization in 6x SSC at about 45ºC followed by one or more washes in 0.1x SSC/0.2% SDS at about 68ºC; or

iv) encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid comprising a nucleotide sequence of SEQ ID NO: 1463 under moderate conditions, wherein the moderate conditions are hybridization in 6x SSC at about 45ºC followed by one or more washes in 0.2x SSC/0.1% SDS at about 42-65ºC;

(b) contacting said sensitized cell with a compound; and

(c) measuring ~~determining the degree to which said compound inhibits~~ the growth of said sensitized cell,

wherein a decrease in growth of said sensitized cell relative to a nonsensitized cell indicates that the compound reduces cellular proliferation.

32. – 44. (canceled)

45. (previously presented) The method of Claim 31, wherein determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a nonsensitized cell comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of said nonsensitized cell.

46. (previously presented) The method of Claim 31, wherein said gene product is from an organism other than *E. coli*.

47. (previously presented) The method of Claim 31, wherein said cell is an organism other than *E. coli*.

48. (previously presented) The method of Claim 31, wherein said sensitized cell is a pathogenic microorganism.

49. (previously presented) The method of Claim 31, wherein said sensitized cell is a Gram positive bacterium.

50. (previously presented) The method of Claim 49, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus* species, *Streptococcus*

species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

51. (previously presented) The method of Claim 50, wherein said bacterium is *Staphylococcus aureus*.

52. (previously presented) The method of Claim 50, wherein said *Staphylococcus* species is coagulase negative.

53. (previously presented) The method of Claim 51, wherein said bacterium is selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

54. (previously presented) The method of Claim 31, wherein said antisense nucleic acid is transcribed from an inducible promoter.

55. (previously presented) The method of Claim 31, further comprising the step of contacting said cell with a concentration of inducer which induces transcription of said antisense nucleic acid to a sublethal level.

56. (previously presented) The method of Claim 31, wherein growth inhibition is measured by monitoring optical density of a culture medium.

57. (previously presented) The method of Claim 31, wherein said gene product is a polypeptide.

58. (previously amended) The method of Claim 57, wherein said gene product is a polypeptide having at least 99% amino acid identity as determined using FASTA version 3.0t78 to SEQ ID NO: 12600.

59. (previously amended) The method of Claim 57, wherein said gene product is a polypeptide having at least 95% amino acid identity as determined using FASTA version 3.0t78 to SEQ ID NO: 12600.

60. (previously amended) The method of Claim 57, wherein said gene product is a polypeptide having at least 90% amino acid identity as determined using FASTA version 3.0t78 to SEQ ID NO: 12600.

61. (previously amended) The method of Claim 57, wherein said gene product is a polypeptide having at least 85% amino acid identity as determined using FASTA version 3.0t78 to SEQ ID NO: 12600.

62. (previously amended) The method of Claim 57, wherein said gene product is a polypeptide having at least 80% amino acid identity as determined using FASTA version 3.0t78 to SEQ ID NO: 12600.

63. (previously amended) The method of Claim 57, wherein said gene product is a polypeptide having at least 70% amino acid identity as determined using FASTA version 3.0t78 to SEQ ID NO: 12600.

64. (previously amended) The method of Claim 57, wherein said gene product is a polypeptide having at least 60% amino acid identity as determined using FASTA version 3.0t78 to SEQ ID NO: 12600.

65. (previously amended) The method of Claim 57, wherein said gene product is a polypeptide having at least 50% amino acid identity as determined using FASTA version 3.0t78 to SEQ ID NO: 12600.

66. (previously amended) The method of Claim 57, wherein said gene product is a polypeptide having at least 40% amino acid identity as determined using FASTA version 3.0t78 SEQ ID NO: 12600.

67. (previously amended) The method of Claim 57, wherein said gene product is a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to SEQ ID NO: 12600.

68. (previously presented) The method of Claim 57, wherein said polypeptide is SEQ ID NO:12600.

69. (previously presented) The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 34% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 12600, a polypeptide having at least 39% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 12600, a polypeptide having at least 42% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 12600 and a polypeptide having at least 43% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 12600.

70. – 76. (canceled)

77. (currently amended) The method of Claim 31, wherein said nucleic acid encoding said gene product with reduced activity or amount is selected from the group consisting of SEQ ID NOs: 4228~~, 6154, 6592, 6872, 7273, 7857,~~ and 8502~~, 9420 and 9605~~.

78. (previously amended) The method of Claim 31, wherein said antisense nucleic acid that reduces activity or amount of said gene product comprises a sequence having at least 97% nucleotide sequence identity to SEQ ID NO: 1463.

79. (previously amended) The method of Claim 31, wherein said antisense nucleic acid that reduces activity or amount of said gene product comprises a sequence having at least 95% nucleotide sequence identity to SEQ ID NO: 1463.

80. (previously amended) The method of Claim 31, wherein said antisense nucleic acid that reduces activity or amount of said gene product comprises a sequence having at least 90% nucleotide sequence identity to SEQ ID NO: 1463.

81. (previously amended) The method of Claim 31, wherein said antisense nucleic acid that reduces activity or amount of said gene product comprises a sequence having at least 85% nucleotide sequence identity to SEQ ID NO: 1463.

82. (previously amended) The method of Claim 31, wherein said antisense nucleic acid that reduces activity or amount of said gene product comprises a sequence having at least 80% nucleotide sequence identity to SEQ ID NO: 1463.

83. (previously amended) The method of Claim 31, wherein said antisense nucleic acid that reduces activity or amount of said gene product comprises a sequence having at least 70% nucleotide sequence identity to SEQ ID NO: 1463.

84. (previously amended) The method of Claim 31, wherein said antisense nucleic acid that reduces activity or amount of said gene product comprises a sequence having at least 70% nucleotide sequence identity to a nucleotide sequence comprising at least 100 consecutive nucleotides of SEQ ID NO: 1463.

85. (previously presented) The method of Claim 12, wherein determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a nonsensitized cell comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of said nonsensitized cell.

86. (previously presented) The method of Claim 12, wherein said prokaryotic organism is either *Staphylococcus aureus* or *Enteroccus faecalis*.

87. (previously amended) The method of Claim 86, wherein said prokaryotic organism is *Staphylococcus aureus* and said antisense nucleic acid is selected from the group consisting of SEQ ID NOs: 1390, 1463, 1845, 2782 and 3283.

88. (canceled)

89. (previously presented) The method of Claim 12, wherein said sensitized cell is a Gram positive bacterium.

90. (previously presented) The method of Claim 89, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

91. (previously presented) The method of Claim 90, wherein said bacterium is *Staphylococcus aureus*.

92. (previously presented) The method of Claim 90, wherein said *Staphylococcus* species is coagulase negative.

93. (previously presented) The method of Claim 91, wherein said bacterium is selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

94. (previously presented) The method of Claim 12, wherein said antisense nucleic acid is transcribed from an inducible promoter.

95. (previously presented) The method of Claim 12, further comprising the step of contacting said cell with a concentration of inducer which induces transcription of said antisense nucleic acid to a sublethal level.

96. (currently amended) The method of Claim 12, wherein ~~growth inhibition~~ cellular proliferation is measured by monitoring optical density of a culture medium.

97. – 99. (canceled)

100. (currently amended) A method for screening a candidate compound for the ability to reduce cellular proliferation comprising the steps of:

(a) providing a sublethal level of an antisense nucleic acid, wherein said antisense nucleic acid reduces the activity or amount of SEQ ID NO:12600, thereby producing a sensitized cell, provided that said sensitized cell is a prokaryotic organism;

(b) contacting said sensitized cell with a compound; and

(c) measuring ~~determining the degree to which said compound inhibits~~ proliferation of said sensitized cell,

wherein a decrease in proliferation of said sensitized cell relative to a nonsensitized cell indicates that the compound reduces cellular proliferation.

101. (previously presented) The method of Claim 48, wherein said pathogenic mircoorganism is selected from the group consisting of *Anaplasma marginale, Aspergillus*

fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata (also called *Torulopsis glabrata*), *Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei, Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis* and any species falling within the genera of any of the above species.

103. (previously presented) The method of Claim 100, wherein said prokaryotic organism is either *Staphylococcus aureus* or *Enteroccus faecalis*.

104. (previously presented) The method of Claim 103, wherein said prokaryotic organism is *Staphylococcus aureus* and said antisense nucleic acid is selected from the group consisting of SEQ ID NOs: 1390, 1463, 1845, 2782 and 3283.

105. (canceled)